Table S1. The comparison of alpha diversity in terms of ACE, Chao1, and Shannon index four study sites. *: significant at 0.05 level; ns: not significant.

	Pairwise comparison	Mean difference	*p* value	Significance	Lower condifence limit	Upper confidence limit
ACE	Dow16_Sed16	-13.667	0.016	*	-24.468	-2.865
	Dow16_Hil16	-9.667	0.077	ns	-20.468	1.135
	Dow16_Up16	-3.667	0.486	ns	-14.468	7.135
	Hil16_Sed16	-4.000	0.448	ns	-14.801	6.801
	Hil16_Up16	6.000	0.259	ns	-4.801	16.801
	Sed16_Up16	10.000	0.068	ns	-0.801	20.801
Chao1	Dow16_Sed16	-15.667	0.005	**	-26.128	-5.205
	Dow16_Hil16	-10.000	0.060	ns	-20.461	0.461
	Dow16_Up16	-4.667	0.362	ns	-15.128	5.795
	Hil16_Sed16	-5.667	0.271	ns	-16.128	4.795
	Hil16_Up16	5.333	0.299	ns	-5.128	15.795
	Sed16_Up16	11.000	0.040	*	0.539	21.461
Shannon	Dow16_Sed16	4.000	0.414	ns	-6.032	14.032
	Dow16_Hil16	-10.000	0.051	ns	-20.032	0.032
	Dow16_Up16	-0.667	0.891	ns	-10.699	9.365
	Hil16_Sed16	14.000	0.009	**	3.968	24.032
	Hil16_Up16	9.333	0.066	ns	-0.699	19.365
	Sed16_Up16	-4.667	0.342	ns	-14.699	5.365

Fig.S1

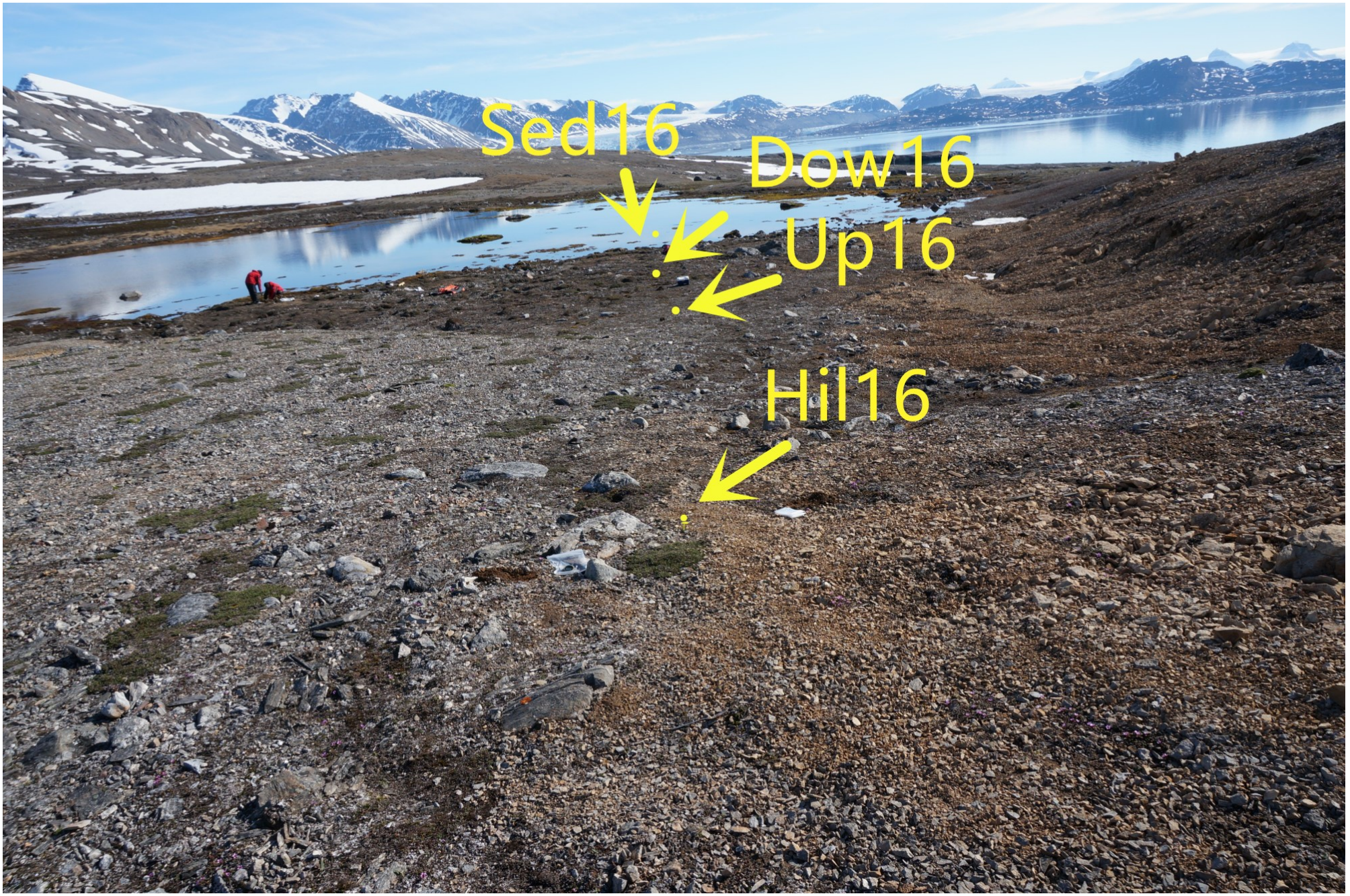


Fig.S2

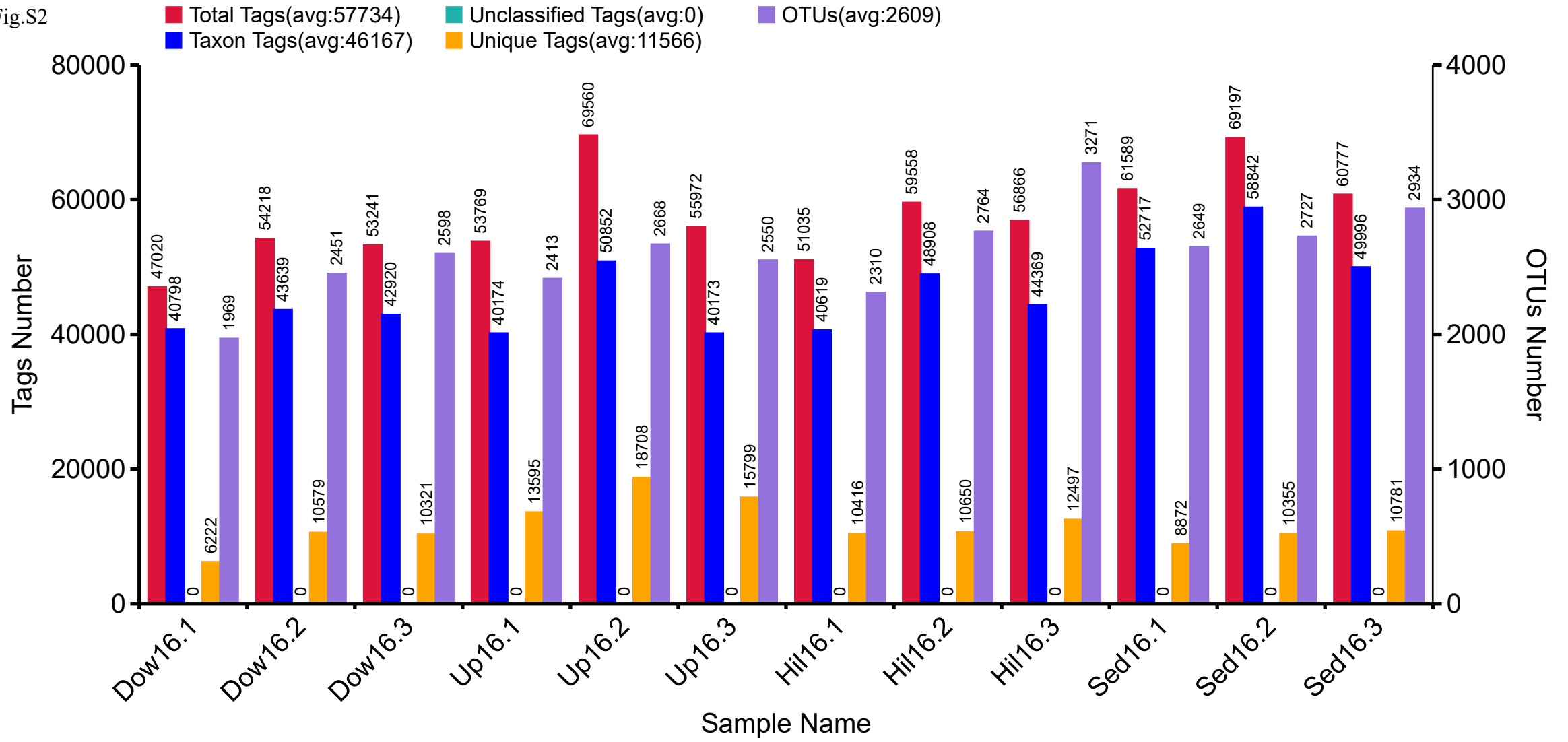
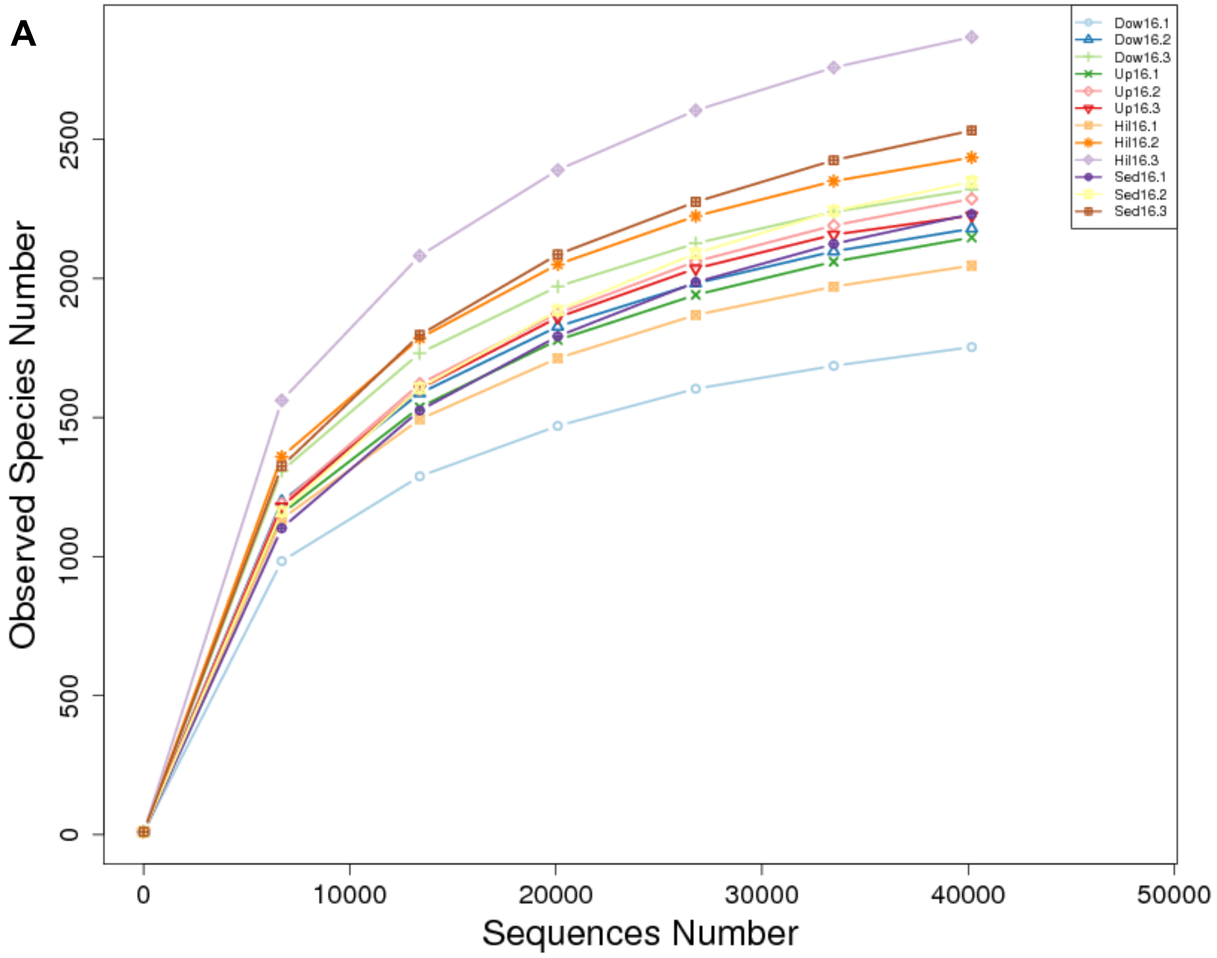

Total Tags(avg:57734)
Taxon Tags(avg:46167)
Unclassified Tags(avg:0)
Unique Tags(avg:11566)
OTUs(avg:2609)
Tags Number
OTUs Number
Sample Name
Dow16.1
Dow16.2
Dow16.3
Up16.1
Up16.2
Up16.3
Hil16.1
Hil16.2
Hil16.3
Sed16.1
Sed16.2
Sed16.3
47020
40798
0
6222
1969
54218
43639
0
10579
2451
53241
42920
0
10321
2598
53769
40174
0
13595
2413
69560
50852
0
18708
2668
55972
40173
0
15799
2550
51035
40619
0
10416
2310
59558
48908
0
10650
2764
56866
44369
0
12497
3271
61589
52717
0
8872
2649
69197
58842
0
10355
2727
60777
49996
0
10781
2934

Fig.S3


A
Observed Species Number
0
500
1000
1500
2000
2500
0
10000
20000
30000
40000
50000
Sequences Number
Dow16.1
Dow16.2
Dow16.3
Up16.1
Up16.2
Up16.3
Hil16.1
Hil16.2
Hil16.3
Sed16.1
Sed16.2
Sed16.3

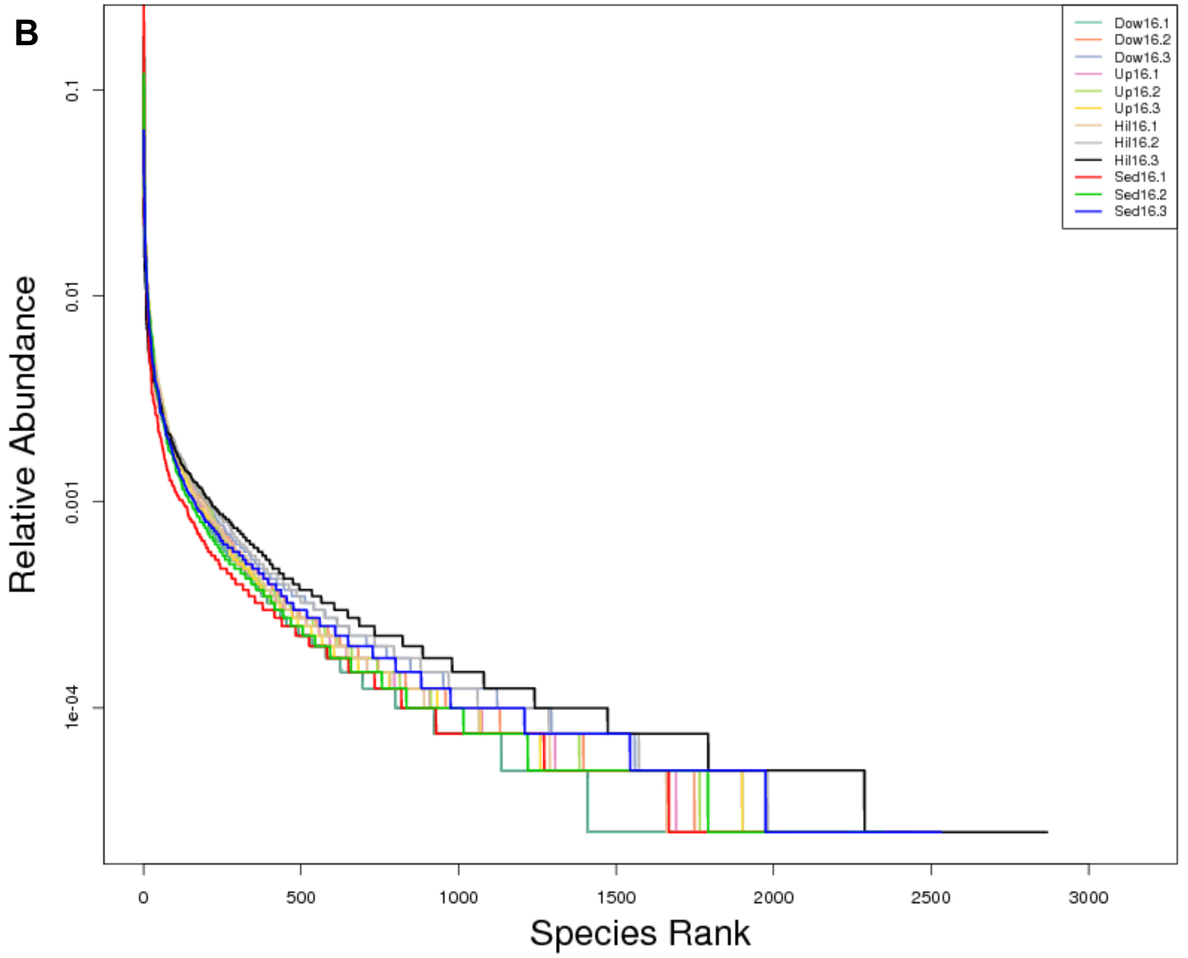

B
Relative Abundance
0.1
0.01
0.001
1e-04
0
500
1000
1500
2000
2500
3000
Species Rank
Dow16.1
Dow16.2
Dow16.3
Up16.1
Up16.2
Up16.3
Hil16.1
Hil16.2
Hil16.3
Sed16.1
Sed16.2
Sed16.3

Fig.S4

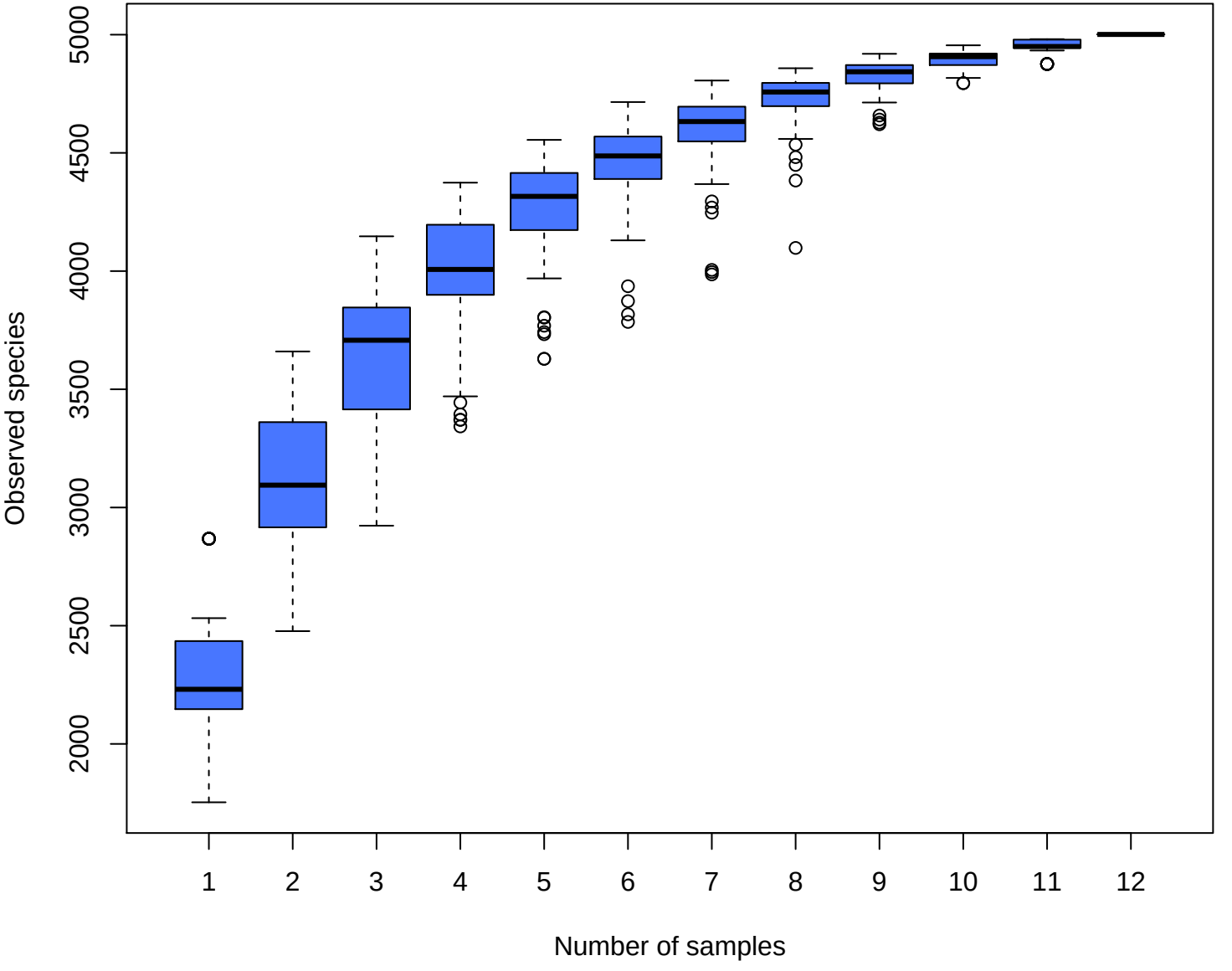

Observed species
2000
2500
3000
3500
4000
4500
5000
1
2
3
4
5
6
7
8
9
10
11
12
Number of samples

Fig.S5

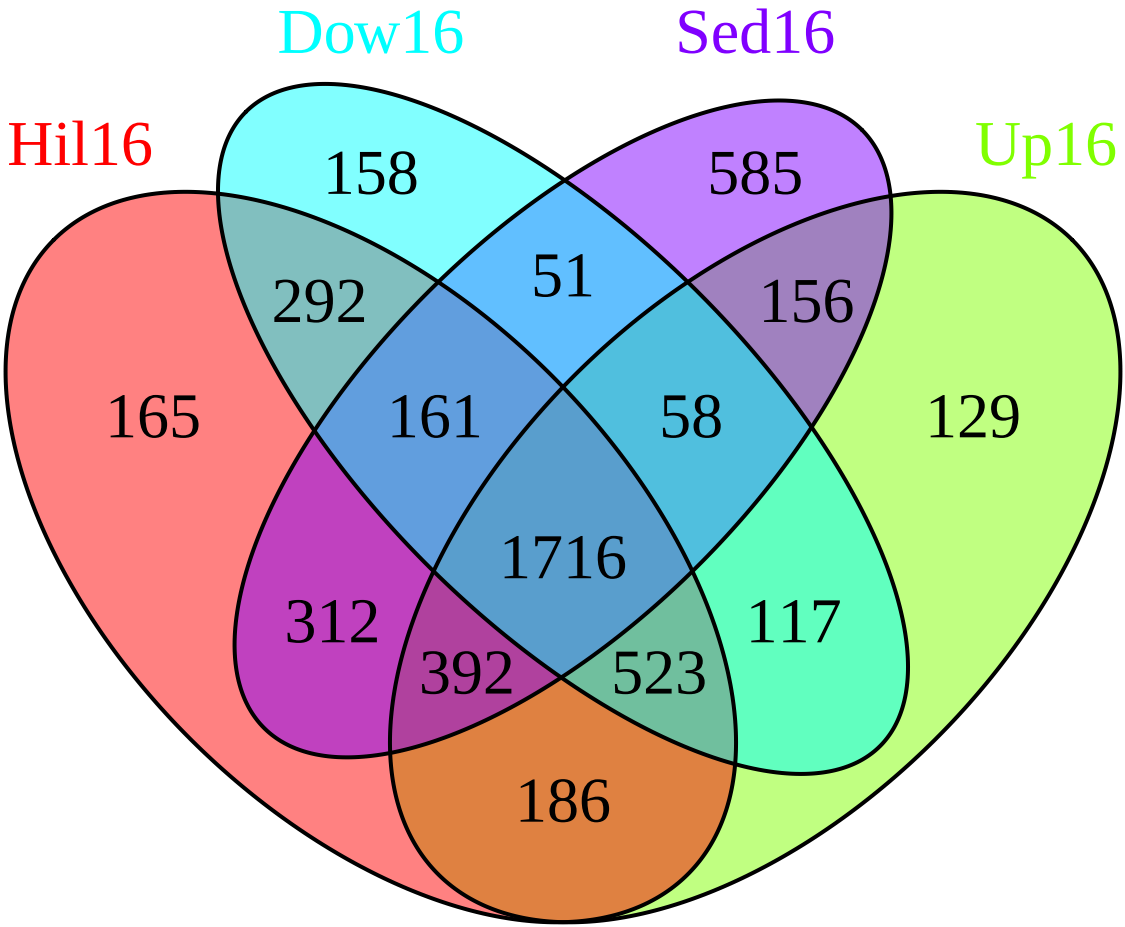
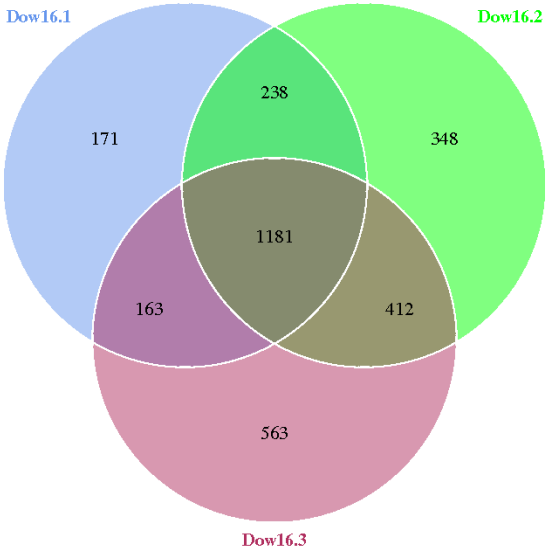
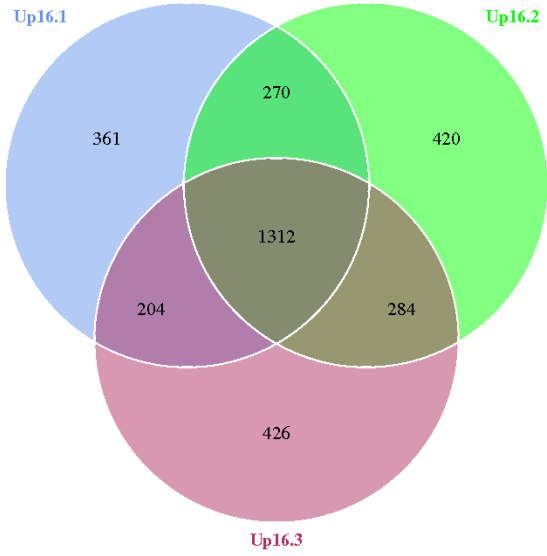
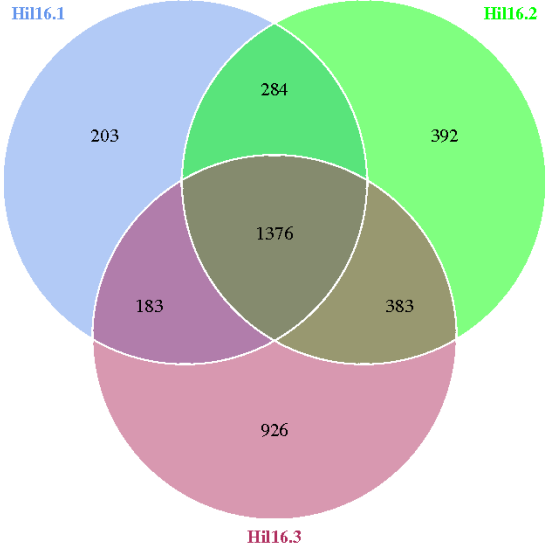

Dow16
Sed16
Hil16
Up16
158
585
292
51
156
165
161
58
129
1716
312
117
392
523
186

Fig.S6


Dow16.1
Dow16.2
Dow16.3
171
238
348
1181
163
412
563


Up16.1
Up16.2
Up16.3
361
270
420
1312
204
284
426


Hil16.1
Hil16.2
Hil16.3
203
284
392
1376
183
383
926

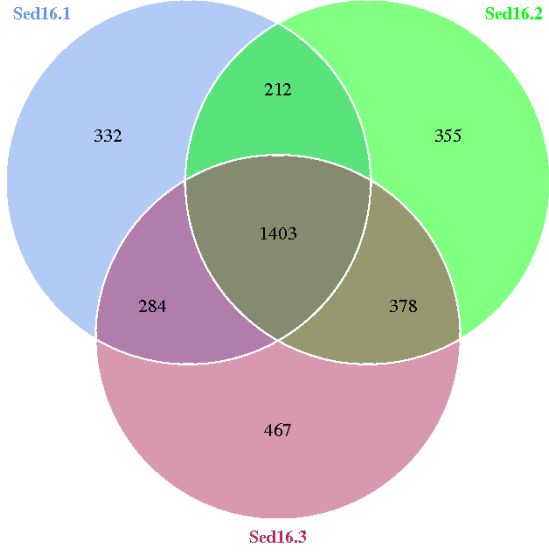

Sed16.1
Sed16.2
Sed16.3
332
212
355
1403
284
378
467

Fig.S7


OTU Tree of Sed16 by GraPhlAn
A:c--Cytophagia
B:o--Cytophagales
C:f--Flammeovirgaceae
D:g--Reichenbachiella
E:c--Bacteroidia
F:c--Betaproteobacteria
G:o--Burkholderiales
H:f--Comamonadaceae
I:o--Rhodocyclales
J:f--Rhodocyclaceae
K:g--Candidatus Accumulibacter
L:g--Dechloromonas
M:c--Epsilonproteobacteria
N:o--Campylobacterales
O:f--Helicobacteraceae
P:g--Sulfuricurvum
Q:c--Gammaproteobacteria
R:o--Methylococcales
S:f--Crenotrichaceae
T:g--Crenothrix
U:c--Alphaproteobacteria
V:o--Sphingomonadales
W:f--Sphingomonadaceae
X:o--Rhizobiales
Y:c--Deltaproteobacteria
Z:o--Desulfobacterales
a:f--Desulfobacteraceae
b:g--Sva0081 sediment group
c:o--43F-1404R
d:c--unidentified Actinobacteria
e:o--Micrococcales
f:c--Methanomicrobia
g:o--Methanosarcinales
h:f--Methanosaetaceae
i:g--Methanosaeta
p--Acidobacteria
p--Bacteroidetes
p--Actinobacteria
p--Proteobacteria
p--Euryarchaeota

Fig.S8


OTU Tree of Hil16 by GraPhlAn
A:c--unidentified Acidobacteria
B:f--unidentified Acidobacteria
C:f--unidentified Acidobacteria
D:o--Subgroup 6
E:f--unidentified Acidobacteria
F:g--unidentified Acidobacteria
G:c--Sphingobacteriia
H:o--Sphingobacteriales
I:c--Betaproteobacteria
J:o--Burkholderiales
K:f--Comamonadaceae
L:f--Alcaligenaceae
M:o--Methylophilales
N:f--Methylophilaceae
O:g--Methylotenera
P:c--Gammaproteobacteria
Q:o--Xanthomonadales
R:c--Alphaproteobacteria
S:o--Sphingomonadales
T:f--Sphingomonadaceae
U:g--Sphingomonas
V:o--Rhodospirillales
W:o--Rhizobiales
X:f--Hyphomicrobiaceae
Y:f--MNG7
Z:f--unidentified Rhizobiales
a:f--Xanthobacteraceae
b:o--Caulobacterales
c:f--Caulobacteraceae
d:c--Deltaproteobacteria
e:c--Thermoleophilia
f:c--unidentified Actinobacteria
g:o--Micrococcales
h:f--Micrococcaceae
i:g--Arthrobacter
j:f--Intrasporangiaceae
k:g--Oryzihumus
p--Acidobacteria
p--Bacteroidetes
p--Actinobacteria
p--Proteobacteria

Fig.S9


OTU Tree of Up16 by GraPhlAn
A:c--unidentified Acidobacteria
B:c--Betaproteobacteria
C:o--Burkholderiales
D:f--Comamonadaceae
E:f--Alcaligenaceae
F:o--Methylophilales
G:f--Methylophilaceae
H:g--Methylotenera
I:c--Gammaproteobacteria
J:o--Xanthomonadales
K:c--Alphaproteobacteria
L:o--Sphingomonadales
M:f--Sphingomonadaceae
N:g--Sphingomonas
O:o--Rhizobiales
P:f--Hyphomicrobiaceae
Q:g--Rhodomicrobium
R:f--MNG7
S:f--unidentified Rhizobiales
T:g--Nordella
U:f--Xanthobacteraceae
V:c--Deltaproteobacteria
W:c--Thermoleophilia
X:o--Solirubrobacterales
Y:c--unidentified Actinobacteria
Z:o--Micromonosporales
a:f--Micromonosporaceae
b:o--Kineosporiales
c:f--Kineosporiaceae
d:g--Kineosporia
e:o--Micrococcales
f:f--Intrasporangiaceae
g:g--Oryzihumus
h:c--Clostridia
i:o--Clostridiales
p--Firmicutes
p--Acidobacteria
p--Bacteroidetes
p--Actinobacteria
p--Proteobacteria

Fig.S10


OTU Tree of Dow16 by GraPhlAn
A:c--unidentified Acidobacteria
B:f--unidentified Acidobacteria
C:f--unidentified Acidobacteria
D:o--Subgroup 6
E:f--unidentified Acidobacteria
F:g--unidentified Acidobacteria
G:c--Cytophagia
H:o--Cytophagales
I:c--Sphingobacteriia
J:o--Sphingobacteriales
K:c--Betaproteobacteria
L:o--Burkholderiales
M:f--Comamonadaceae
N:f--Alcaligenaceae
O:o--Methylophilales
P:f--Methylophilaceae
Q:g--Methylotenera
R:c--Gammaproteobacteria
S:o--Xanthomonadales
T:f--Xanthomonadaceae
U:c--Alphaproteobacteria
V:o--Sphingomonadales
W:f--Sphingomonadaceae
X:g--Sphingomonas
Y:o--Rhizobiales
Z:f--Hyphomicrobiaceae
a:f--MNG7
b:f--Xanthobacteraceae
c:o--Caulobacterales
d:c--Deltaproteobacteria
e:c--unidentified Actinobacteria
f:o--Micrococcales
g:f--Micrococcaceae
h:g--Arthrobacter
i:f--Intrasporangiaceae
j:g--Oryzihumus
p--Acidobacteria
p--Bacteroidetes
p--Actinobacteria
p--Proteobacteria
p--Thaumarchaeota